

GenCore version 5.1.3  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: January 16, 2003, 16:55:57 ; Search time 440.214 Seconds  
(without alignments)  
330.553 Million cell updates/sec

Title: US-09-856-070-16  
Project score: 25  
Sequence: 1 EREKE 5

Scoring table: BLOSUM62

Xgapop 10.0 ; Xgapext 0.5  
Ygapop 10.0 ; Ygapext 0.5  
Fgapop 6.0 ; Fgapext 7.0  
Delop 6.0 ; Delext 7.0

Searched: 2054640 seqs, 1455402878 residues

Total number of hits satisfying chosen parameters: 4100000

Minimum DR seq length: 0

Maximum DR seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-Model=frame\_plus\_p2n\_model -DEV=exp  
-O=/cgn2\_1/psp/seqs/US09856070/blast\_14012003\_155664\_1661/app\_query\_blast\_1\_1592  
-DB=GenEmbl -QMT=fastlap -SUFFIX=cpe -MINMATCH=0.1 -LOCAL=1.0 -DELPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40 cdi -LIST=45  
-DOCALIGN=206 -THR\_SCOPE=opt -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-CURRMT=trc -NMM=ext -HAPASIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USP=US09856070 -ARGN\_1=US941 -ARGN\_2=14012003\_155664\_1661 -NTERM=6 -LTERM=3  
-NO\_XLPXY -NO\_WMAP -IARGQUERYF -NEG\_SCORES=0 -WALL -LUNNOR -REV\_TIMEOUT=120  
-WARN\_TIMEOUT=30 -THREAS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7  
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database

Genbank

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_em:\*
- 5: gb\_ov:\*
- 6: gb\_paf:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vl:\*
- 15: gb\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_mu:\*
- 21: em\_of:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_pl:\*
- 25: em\_ro:\*
- 26: em\_sts:\*
- 27: em\_un:\*
- 28: em\_un:\*

- 29: em\_vl:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pin:\*
- 35: em\_htg\_rnd:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgo\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Match Length	DB ID	Description
1	25	100.0	22	AF089230	AF089230 Sequence
2	25	100.0	22	AF158374	AF158374 Sequence
3	25	100.0	22	AF172577	AF172577 Sequence
4	25	100.0	25	AF137561	AF137561 Sequence
5	25	100.0	25	AF139667	AF139667 Sequence
6	25	100.0	47	AX378317	AX378317 Sequence
7	25	100.0	58	AR208349	AR208349 Sequence
8	25	100.0	60	S44200	S44200 class VI 2y
9	25	100.0	61	AF062766	AF062766 glycine m
10	25	100.0	62	AF164071	AF164071 Caprolin
11	25	100.0	64	AF164071	L29950 Human STS U
12	25	100.0	65	AX481825	AX481825 Sequence
13	25	100.0	67	AX481825	AX481825 M.musculus
14	25	100.0	79	MMNCDS2b	MMNCDS2b
15	25	100.0	83	AX240980	AX240980 Sequence
16	25	100.0	83	AFH43703	AFH43703 Arabidops
17	25	100.0	84	AF120076S4	AF120076 Mus muscu
18	25	100.0	87	AF033554	AF033554 Pyliloso
19	25	100.0	91	MMB18061	X55201 M.musculus
20	25	100.0	95	U0075301A	L30827 Human STS U
21	25	100.0	96	AF411909	AF411909 Formica e
22	25	100.0	100	AF411993	AF411993 Formica e
23	25	100.0	102	AF317797	AF317797 Elephas m
24	25	100.0	103	AY074720	AY074720 Prunus av
25	25	100.0	110	AF317798	AF317798 Elephas m
26	25	100.0	110	AF317799	AF317799 Loxodonta
27	25	100.0	110	AF317800	AF317800 Loxodonta
28	25	100.0	111	AF155792	AF155792 Saccopier
29	25	100.0	111	HUMHBLAP	H45431 Human micro
30	25	100.0	112	AF317793	AF317793 Mammothus
31	25	100.0	112	AF317794	AF317794 Mammothus
32	25	100.0	112	AF317795	AF317795 Mammothus
33	25	100.0	112	AF317796	AF317796 Mammothus
34	25	100.0	113	A0028712	A0028712 Rattus no
35	25	100.0	115	AC0420073	AJ420073 Anopheles
36	25	100.0	115	HS155H6F	254658 H.sapiens C
37	25	100.0	116	CECALE037	X86204 C.familia
38	25	100.0	119	AF114759	AF114759 Icterus
39	25	100.0	119	AF200944	AF200944 Meriones
40	25	100.0	120	AF226045	AF226045 Passaria
41	25	100.0	120	Y02294SL1	AY021303 Homo sapi
42	25	100.0	123	U040324	G44024 WIAP 1654-S
43	25	100.0	123	U040325	G44025 WIAP 1654-S
44	25	100.0	123	U040326	G44026 WIAP 1654-S
45	25	100.0	126	U040327	G01146 human STS S

ALIGNMENTS

RESULT 1

AK089240  
LOCUS AK089240  
DEFINITION Sequence 19 from patent US 5994062.  
ACCESSION AK089240  
VERSION AK089240.1 GI:10015487  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Mulshine, J.L. and Lockman, M.S.  
TITLE Epithelial protein and DNA thereof for use in early cancer detection  
JOURNAL Patent: US 5994062-A 19 30-NOV-1999;  
FEATURES Location/Qualifiers  
source 1..22  
BASE COUNT 10 a 3 c 7 q 2 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 31.6 Length: 22  
Score: 25.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-856-070-16 (1-5) x AK089240 (1-22)  
QY 1 GluArgGluLysGlu 5  
Db 1 GACAGAGAGAAAGGAA 15  
RESULT 2  
LOCUS AK158374  
DEFINITION Sequence 19 from patent US 6251586.  
ACCESSION AK158374  
VERSION AK158374.1 GI:16220396  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Mulshine, J.L. and Lockman, M.S.  
TITLE Epithelial protein and DNA thereof for use in early cancer detection  
JOURNAL Patent: US 6251586-A 19 26-JUN-2001;  
FEATURES Location/Qualifiers  
source 1..22  
BASE COUNT 10 a 3 c 7 q 2 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 31.6 Length: 22  
Score: 25.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-856-070-16 (1-5) x AK158374 (1-22)  
QY 1 GluArgGluLysGlu 5  
Db 1 GACAGAGAGAAAGGAA 15  
RESULT 4  
LOCUS AK172577  
DEFINITION Sequence 47 from patent US 6200803.  
ACCESSION AK172577  
VERSION AK172577.1 GI:14481412  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Robertis, C.J.  
TITLE Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs  
JOURNAL Patent: US 6197517-A 47 06-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..25  
BASE COUNT 4 a 8 c 1 q 12 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 36.1 Length: 25  
Score: 25.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-856-070-16 (1-5) x AK172577 (1-25)  
QY 1 GluArgGluLysGlu 5  
Db 19 GACAGAGAGAAAGGAG 5  
RESULT 5  
LOCUS AK139067  
DEFINITION Sequence 47 from patent US 6200803.  
ACCESSION AK139067  
VERSION AK139067.1 GI:14481412  
KEYWORDS

ACCESSION AK172577  
VERSION AK172577.1 GI:14481412  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 22)  
AUTHORS Re, R. and Cook, J.  
TITLE Inhibition of cellular proliferation in vitro by oligonucleotide binding to a chromosomal binding site for p53 protein  
JOURNAL Patent: US 6303328-A 9 16-OCT-2001;  
FEATURES Location/Qualifiers  
source 1..22  
BASE COUNT 0 a 7 c 0 q 15 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 31.6 Length: 22  
Score: 25.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-856-070-16 (1-5) x AK172577 (1-22)  
QY 1 GluArgGluLysGlu 5  
Db 22 GAAAGAGAGAAAGGAA 8  
RESULT 4  
LOCUS AK137561  
DEFINITION Sequence 47 from patent US 6197517.  
ACCESSION AK137561  
VERSION AK137561.1 GI:14479070  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 25)  
AUTHORS Robertis, C.J.  
TITLE Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs  
JOURNAL Patent: US 6197517-A 47 06-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..25  
BASE COUNT 4 a 8 c 1 q 12 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 36.1 Length: 25  
Score: 25.00 Matches: 5  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 6 Gaps: 0  
US-09-856-070-16 (1-5) x AK137561 (1-25)  
QY 1 GluArgGluLysGlu 5  
Db 19 GACAGAGAGAAAGGAG 5  
RESULT 5  
LOCUS AK139067  
DEFINITION Sequence 47 from patent US 6200803.  
ACCESSION AK139067  
VERSION AK139067.1 GI:14481412  
KEYWORDS

SOURCE: Unknown.  
 ORGANISM: Unknown.  
 REFERENCE: 1 (bases 1 to 25)  
 AUTHORS: Robert, C.J.  
 TITLE: Essential genes of yeast as targets for antifungal agents, herbicides, insecticides and anti-proliferative drugs  
 JOURNAL: Patent: US 620803-A 47 13-MAR-2001.  
 FEATURES: Location/Qualifiers  
 SOURCE: 1..25  
 BASE COUNT: 4 a 8 c 1 g 12 t  
 ORIGIN: 1..25  
 Alignment Scores:  
 Pred. No.: 36.1 Length: 25  
 Score: 25.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-856-070-16 (1-5) x APL30067 (1-25)  
 QY 1 GluArgGluLysGlu 5  
 Db 19 GAGAGAGAAAGAGAG 5  
 RESULT 6  
 LOCUS AX378317/c 47 bp DNA linear PAT 18-MAR-2002  
 DEFINITION Sequence 106 from Patent W00206525.  
 ACCESSION AX378317  
 VERSION AX378317.1 GI:19574167  
 KEYWORDS human.  
 SOURCE: Homo sapiens  
 ORGANISM: Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates, Catarrhini; Hominoidea; Homo  
 REFERENCE: 1  
 AUTHORS: Cohen, D., Blumenfeld, M., Chumakov, I., Abderrahim, H. and Bihaoui, R.  
 TITLE: Obesity associated bi-allelic marker maps  
 JOURNAL: Patent: WO 0206525-A 106 24-JAN-2002;  
 GENSET (FR)  
 FEATURES: Location/Qualifiers  
 SOURCE: 1..47  
 variation /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT: 8 a 13 c 2 g 23 t 1 others  
 ORIGIN: 1..47  
 Alignment Scores:  
 Pred. No.: 69.8 Length: 47  
 Score: 25.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-856-070-16 (1-5) x AX378317 (1-47)  
 QY 1 GluArgGluLysGlu 5  
 Db 18 GAAAGAGAGAAAGAG 4  
 RESULT 7  
 LOCUS AR208349/c 58 bp DNA linear PAT 20-JUN-2002  
 DEFINITION Sequence 5 from patent US 6383747.  
 ACCESSION AR208349  
 VERSION AR208349.1 GI:21509480

KEYWORDS: Unknown.  
 SOURCE: Unknown.  
 ORGANISM: Unknown.  
 REFERENCE: 1 (bases 1 to 58)  
 AUTHORS: Dawkins, R. Letts, and Abraham, L. Joseph.  
 TITLE: Method for determining ancestral haplotypes using haplo-specific genetic elements within the major histocompatibility complex multigene cluster  
 JOURNAL: Patent: US 648747-A 5 07-MAY-2002.  
 FEATURES: Location/Qualifiers  
 SOURCE: 1..58  
 BASE COUNT: 1 a 27 c 0 g 30 t  
 ORIGIN: 1..58  
 Alignment Scores:  
 Pred. No.: 87 Length: 58  
 Score: 25.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0  
 US-09-856-070-16 (1-5) x AR208349 (1-58)  
 QY 1 GluArgGluLysGlu 5  
 Db 50 GAGAGAGAAAGAG 36  
 RESULT 8  
 LOCUS S44200 60 bp mRNA linear PLN 08-MAY-1993  
 DEFINITION class VI zygote specific cell wall hydroxyproline-rich glycoprotein [Chlamydomonas reinhardtii, mRNA Partial, 60 nt].  
 ACCESSION S44200  
 VERSION S44200.1 GI:255403  
 KEYWORDS Chlamydomonas reinhardtii.  
 ORGANISM: Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadales; Chlamydomonas.  
 REFERENCE: 1 (bases 1 to 60)  
 AUTHORS: Woessner, J. P. and Goodenough, U. W.  
 TITLE: Molecular characterization of a zygote wall protein: an extensin-like molecule in Chlamydomonas reinhardtii  
 JOURNAL: Plant Cell 1 (9), 901-911 (1989)  
 MEDLINE 92393420  
 PUBMED 2535530  
 REMARK: GenBank Staff at the National Library of Medicine created this entry (NCBI gbbseq 113226) from the original journal article. This sequence comes from Fig. 6  
 FEATURES: Location/Qualifiers  
 SOURCE: 1..60  
 /organism="Chlamydomonas reinhardtii"  
 /db\_xref="taxon:3055"  
 gene: 1..60  
 /partial  
 /gene="class VI zygote specific cell wall hydroxyproline-rich glycoprotein"  
 CDS: 1..60  
 /partial  
 /gene="class VI zygote specific cell wall hydroxyproline-rich glycoprotein"  
 /note="This sequence comes from Fig. 6"  
 /codon\_start=1  
 /protein\_id="AA023259.1"  
 /db\_xref="GI:255404"  
 /translation="ATPSPSPSPSPSPSPSPA"  
 BASE COUNT: 3 a 35 c 5 g 17 t  
 ORIGIN: 1..60  
 Alignment Scores:

Prod. No.: 90-2  
Score: 25.00  
Length: 60  
Matches: 5  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatches: 0  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

US 09 856-070-16 (1-5) x S44200 (1-60)

QY 1 GluArqGluLysGlu 5

|||||

DB 43 GAGAGAGAGAGAGAG 29

RESULT 9

AF062766

LOCUS AF062766 61 bp DNA linear PLN 20-APR-2001

DEFINITION Glycine max microsatellite A653 repeat region.

ACCESSION AF062766

VERSION AF062766.1 GI:3372763

KEYWORDS

SOURCE Glycine max.

ORGANISM Glycine max.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 61)

AUTHORS Peakall, R., Gilmore, S., Keys, W., Morgante, M. and Rafalski, A.

TITLE Cross-species amplification of soybean (Glycine max) simple

sequence repeats (SSRs) within the genus and other legume genera:

Implications for the transferability of SSRs in plants

Mol. Biol. Evol. 15 (10): 1275-1287 (1998)

JOURNAL 99004702

PubMed 9787434

REFERENCE 2 (bases 1 to 61)

AUTHORS Peakall, R., Gilmore, S., Keys, W., Morgante, M. and Rafalski, A.

TITLE Direct Submission

Submitted (04 MAY 1998) Division of Botany and Zoology, Australian

National University, Canberra, ACT 0200, Australia

FEATURES

Location/Qualifiers

1..61

/organism="Glycine max"

/db\_xref="taxon:3847"

repeat\_region 1..40

/note="microsatellite A653"

/rpt\_type=tandem

/rpt\_unit=ag

BASE COUNT 29 a 2 c 25 g 5 t

ORIGIN

Alignment Scores:  
Prod. No.: 91-7  
Score: 25.00  
Length: 61  
Matches: 5  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatches: 0  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

US 09 856-070-16 (1-5) x AF062766 (1-61)

QY 1 GluArqGluLysGlu 5

|||||

DB 23 GAGAGAGAGAGAGAG 47

RESULT 10

AF164071

LOCUS AF164071 62 bp DNA linear MAM 21 OCT 2000

DEFINITION Capreolus capreolus microsatellite sequence.

ACCESSION AF164071

VERSION AF164071.1 GI:10944318

KEYWORDS

SOURCE Capreolus capreolus.

ORGANISM Capreolus capreolus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;  
Cervidae; Odocoileinae; Capreolus.

REFERENCE 1 (bases 1 to 62)

AUTHORS Fickel, J. and Reinsch, A.

TITLE Microsatellite sequences as genetic markers in European Roe deer

JOURNAL Unpublished

PPFPFNF 2 (bases 1 to 62)

AUTHORS Fickel, J. and Reinsch, A.

TITLE Direct Submission

Submitted (02-JUL-1999) Evolutionary Genetics, Institute for Zoo

Biology and Wildlife Research, Alfred Kowale-Str. 17, Berlin

FEATURES

Location/Qualifiers

1..62

/organism="Capreolus capreolus"

/db\_xref="taxon:9858"

/note="blood"

repeat\_region 21..30

/note="microsatellite"

/rpt\_type=tandem

/rpt\_unit=qt

repeat\_region 31..38

/note="microsatellite"

/rpt\_type=tandem

/rpt\_unit=atgt

repeat\_region 43..54

/note="microsatellite"

/rpt\_type=tandem

/rpt\_unit=ga

BASE COUNT 22 a 4 c 20 g 15 t 1 others

ORIGIN

Alignment Scores:  
Prod. No.: 93-3  
Score: 25.00  
Length: 62  
Matches: 5  
Percent Similarity: 100.00%  
Conservative: 0  
Best Local Similarity: 100.00%  
Mismatches: 0  
Query Match: 100.00%  
Indels: 0  
Gaps: 0

US-09-856-070-16 (1-5) x AF164071 (1-62)

QY 1 GluArqGluLysGlu 5

|||||

DB 47 GAGAGAGAGAGAGAG 61

RESULT 11

HUMUT272A

LOCUS HUMUT272A Human STS UT272, 5' primer bind, sequence tagged site. 64 bp DNA linear STS 04-AUG-1994

DEFINITION Human STS UT272, 5' primer bind, sequence tagged site.

ACCESSION L29950

VERSION L29950.1 GI:521225

KEYWORDS STS, PCR primer, SLS sequence, microsatellite, DNA, microsatellite

marker, repeat polymorphism, sequence tagged site.

SOURCE Homo sapiens

ORGANISM Homo sapiens

REFERENCE

AUTHORS

White, R.

Genetic and physical mapping of simple sequence repeat containing

sequence tagged sites from the human genome

Unpublished (1994)

Submitted by: Utah Center for Human Genome Research University of

Utah, Dept. of Human Genetics

2160 Eccles Institute of Human Genetics

Salt Lake City, UT 84112

e-mail: sts@corona.med.utah.edu

Primer A: GGGCAGAGAGAGAGAGAG

Primer B: CCAGATACGGGGCCACAGA

End to Label: Primer A

PCR Profile:

Initial Denaturation: 94C 360sec

Cycles Denaturation Annealing

C 10 sec: 65 C 10 sec 72 C 20 sec Mg<sup>2+</sup> 2.00 mM

Gel: Acrylamide 7%, Formamide 32%, Urea 14%

Alleles: 1.

Location/Qualifiers

1. .64

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/map="17"

1. .123

/evidence=experimental

30 a 5 c 23 g 6 t

primer\_bind

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 96.5

Score: 25.00

Length: 64

Matches: 5

Conservative: 0

Best Local Similarity: 100.00%

Mismatch: 0

Query Match: 100.00%

Indels: 0

Gaps: 0

DB: 11

US-09-856-070-16 (1-5) x HUMH1Z72A (1-64)

QY 1 GluArgGluLysGlu 5

DB 31 GAAACAGACAAAGAG 45

RESULT 12

AX483825/c

DEFINITION

Sequence 1125 from Patent WO00053738.

ACCESSION

AX483825

VERSION

AX483825.1

KEYWORDS

Candida albicans.

SOURCE

Candida albicans.

ORGANISM

Eukaryota, Fungi, Ascomycota, Saccharomycotina; Saccharomycetes;

Saccharomycetales, mitosporic Saccharomycetales; Candida.

REFERENCE

Boomer, T., Jiang, P., Rupp, C., Bussey, H. and Chises, K. I.

Gene disruption methodologies for drug target discovery

Patent: WO 0054728-A 1125 11-11-2002

Elitra pharmaceuticals, Inc. (US)

FEATURES

Location/Qualifiers

1. .65

/organism="Candida albicans"

/db\_xref="taxon:5476"

18 a 10 c 4 g 33 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 98

Score: 25.00

Length: 65

Matches: 5

Conservative: 0

Best Local Similarity: 100.00%

Mismatch: 0

Query Match: 100.00%

Indels: 0

Gaps: 0

DB: 6

US-09-856-070-16 (1-5) x AX483825 (1-65)

QY 1 GluArgGluLysGlu 5

DB 34 GAGACAGACAAAGAG 20

RESULT 13

MMUNDS26

LOCUS

DEFINITION

ACCESSION

X55244

VERSION

X55244.1

KEYWORDS

microsatellite DNA.

SOURCE

Mus musculus.

ORGANISM

Mus musculus.

REFERENCE

1 (bases 1 to 67)

AUTHORS

Cornall, R.J., Altman, T.J., Hearne, C.M. and Todd, J.A.

TITLE

The generation of a library of PCR-analysed microsatellite variants for genetic mapping of the mouse genome

JOURNAL

Genomics 10 (4): 874-881 (1991)

MEDLINE

92009923

PUBMED

1916820

REFERENCE

2 (bases 1 to 67)

AUTHORS

Cornell, R.C., Altman, T.J., Hearne, C.M. and Todd, J.A.

TITLE

The Generation of a Library of PCR-Analysed Microsatellite Variants for Genetic Mapping of the Mouse Genome

JOURNAL

Unpublished

FEATURES

Location/Qualifiers

1. .67

/organism="Mus musculus"

/strain="NOD, ssp.domesticus"

/db\_xref="taxon:10090"

1. .67

/note="D0nds26"

26 a 11 c 20 g 10 t

BASE COUNT

ORIGIN

Alignment Scores:

Pred. No.: 101

Score: 25.00

Length: 67

Matches: 5

Conservative: 0

Best Local Similarity: 100.00%

Mismatch: 0

Query Match: 100.00%

Indels: 0

Gaps: 0

DB: 10

US-09-856-070-16 (1-5) x MMUNDS26 (1-67)

QY 1 GluArgGluLysGlu 5

CT 16 CAGAGAGGAAAGAG 59

RESULT 14

PF1R3

LOCUS

PF1R3

DEFINITION

Bacteriophage 11 3'-terminal region rna.

ACCESSION

J02452

VERSION

J02452.1

KEYWORDS

fi rna from e.coli a/lambda.

ORGANISM

Bacteriophage FI

REFERENCE

Viruses: ssRNA positive-strand viruses, no DNA stage; Leviviridae;

Allolevivirus; Allolevivirus subgroup IV.

1 (bases 1 to 78)

AUTHORS

Inokuchi, Y., Hirashima, A. and Watanabe, I.

TITLE

Comparison of the nucleotide sequences at the 3' terminal region of RNAs from RNA coliphages

J. Mol. Biol. 158 (4): 711-730 (1982)

MEDLINE

83010413

PUBMED

7120417

FEATURES

Location/Qualifiers

1. .78

/organism="Bacteriophage FI"

/db\_xref="taxon:11993"

18 a 27 c 17 g 16 t

BASE COUNT

ORIGIN

Alignment Scores:  
 Pred. No.: 119 Length: 78  
 Score: 25.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 7 Gaps: 0

US 09-856-070-16 (1-5) x PFTR3 (1-78)

QY 1 GluArgGlnLysGlu 5  
 |||||  
 DB 10 GAGACAGAGAAAGAA 24

# RESULT 15

AX240980/c

LOCUS AX240980 24 bp DNA linear PAT 26-SEP-2001

DEFINITION Sequence 218 from Patent WO0160975.

ACCESSION AX240980

VERSION AX240980.1 GI:15797855

KEYWORDS

SOURCE synthetic construct.

ORGANISM synthetic construct.

artificial sequences.

REFERENCE 1 (bases 1 to 83)

AUTHORS Roemer, T., Jiang, B., Roemer, C. and Hussey, H.

TITLE Gene disruption methodologies for drug target discovery

JOURNAL Patent: WO 0160975-A 218 23-AUG-2001;

Elitra Pharmaceuticals, Inc. (US)

FEATURES Location/Qualifiers

Source  
 1..83  
 /organism="synthetic construct"  
 /db\_xref="taxon:3263"  
 /note="DNA primer"

BASE COUNT 21 a 14 c 11 g 37 t

ORIGIN

Alignment Scores:  
 Pred. No.: 127 Length: 83  
 Score: 25.00 Matches: 5  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 6 Gaps: 0

US 09-856-070-16 (1-5) x AX240980 (1-83)

QY 1 GluArgGlnLysGlu 5  
 |||||  
 DB 34 GAGACAGAGAAAGAG 20

Search completed: January 16, 2003, 19:02:22  
 Job time : 444,214 secs